SEQUENCE LISTING

<110> HONJO, TASUKU
KATO, KEIZO
TADA, HIDEAKI

<120> POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM

<130> Q58771

<140> 09/529,064
<141> 2000-04-07

<150> PCT/JP98/04515
<151> 1998-10-06

<150> HEI-9-274673
<151> 1997-10-07

<160> 28

<170> PatentIn Ver. 2.1

<210> 1
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<400> 1

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  1               5                  10                  15

Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
             20                  25                  30

Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
         35                  40                  45

Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
     50                  55                  60

Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
 65                  70                  75                  80

Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
                 85                  90                  95

Val Asn Thr Ser Ile Pro Phe Ser Phe Glu Gly Ile Leu Phe Pro Lys
            100                 105                 110

Gly His Tyr Arg Cys Val Ala Glu Ala Ile Ala Gly Asp Thr Glu Glu
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Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile His Arg Arg Asp Val Asn
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<213> Mus musculus

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aaattcccta tttcaattag ttctgaaccc tgcataagac tgaggggaac caatggattt 180
gtgcatgttg agttcattcc aagaggaaac ttaaaatatt tatatttcaa cctattcatc 240
agtgtcaact ccatagagtt gccgaagcgt aaggaagttc tgtgccatgg acatgatgat 300
gactattctt tttgcagagc tctgaaagga gagactgtga atacatcaat accattctct 360
ttcgagggaa tactatttcc taagggccat tacagatgtg ttgcagaagc tattgctggg 420
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<210> 3
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<212> DNA
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<220>
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<222> (23)..(70)

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<222> (71)..(502)

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ctt tct ccc ata ttg act gaa tct gag aag caa cag tgg ttc tgc aac 100
Leu Ser Pro Ile Leu Thr Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn
-5 -1 1 5 10

tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
15 20 25

cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
30 35 40

gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
45 50 55

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tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt   292
Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
     60                  65                  70

aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga   340
Lys Glu Val Leu Cys His Gly His Asp Asp Asp Tyr Ser Phe Cys Arg
 75                  80                  85                  90

gct ctg aaa gga gag act gtg aat aca tca ata cca ttc tct ttc gag   388
Ala Leu Lys Gly Glu Thr Val Asn Thr Ser Ile Pro Phe Ser Phe Glu
                95                 100                 105

gga ata cta ttt cct aag ggc cat tac aga tgt gtt gca gaa gct att   436
Gly Ile Leu Phe Pro Lys Gly His Tyr Arg Cys Val Ala Glu Ala Ile
            110                 115                 120

gct ggg gat act gaa gaa aag ctc ttc tgt ttg aat ttc acc atc att   484
Ala Gly Asp Thr Glu Glu Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile
        125                 130                 135

cac cgc cgt gat gtc aat tagaatatgc tgaatacaca cacacacaca          532
His Arg Arg Asp Val Asn
    140

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aaaaaaaaaa aaaaaa                                                 608


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<212> PRT
<213> Mus musculus

<400> 4
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Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn Ser Ser Asp Ala Ile Ile
  1                5                  10                  15

Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
             20                  25                  30

Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
         35                  40                  45

Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
     50                  55                  60

Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
 65                  70                  75                  80

Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Gly Tyr
                85                  90                  95

Ala Ile
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<210> 5
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<212> DNA
<213> Mus musculus

<400> 5
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aaattcccta tttcaattag ttctgaaccc tgcataagac tgaggggaac caatggattt 180
gtgcatgttg agttcattcc aagaggaaac ttaaaatatt tatatttcaa cctattcatc 240
agtgtcaact ccatagagtt gccgaagcgt aaggaagttc tgtgccatgg acatgatgat 300
gactattctt tttgcagagc tctgaaagga ggatatgcta tt 342

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<212> DNA
<213> Mus musculus

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<220>
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<222> (23)..(364)

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ctt tct ccc ata ttg act gaa tct gag aag caa cag tgg ttc tgc aac 100
Leu Ser Pro Ile Leu Thr Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn
-5 -1 1 5 10

tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
15 20 25

cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
30 35 40

gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
45 50 55

tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt 292
Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
60 65 70

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aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga   340
Lys Glu Val Leu Cys His Gly His Asp Asp Asp Tyr Ser Phe Cys Arg
 75                  80                  85                  90

gct ctg aaa gga gga tat gct att tagaaaatat gagactgtga atacatcaat  394
Ala Leu Lys Gly Gly Tyr Ala Ile
                95

accattctct ttcgagggaa tactatttcc taagggccat tacagatgtg ttgcagaagc 454

tattgctggg gatactgaag aaaagctctt ctgtttgaat ttcaccatca ttcaccgccg 514

tgatgtcaat tagaatatgc tgaatacaca cacacacaca cacacacaca cacacatatg 574

tatatatata ttttttttacc ccaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa     630


<210> 7
<211> 160
<212> PRT
<213> Homo sapiens

<400> 7
Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
    -15                 -10                  -5                  -1

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
  1                5                  10                  15

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
             20                  25                  30

Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys Gly Leu Leu His Ile Phe
         35                  40                  45

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
     50                  55                  60

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
 65                  70                  75                  80

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
                 85                  90                  95

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
            100                 105                 110

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
        115                 120                 125

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
    130                 135                 140


<210> 8
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<212> DNA
<213> Homo sapiens
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caatacccaa tttcaattaa tgttaacccc tgtatagaat tgaaaggatc caaaggatta 180
ttgcacattt tctacattcc aaggagagat ttaaagcaat tatatttcaa tctctatata 240
actgtcaaca ccatgaatct tccaaagcgc aaagaagtta tttgccgagg atctgatgac 300
gattactctt tttgcagagc tctgaaggga gagactgtga atacaacaat atcattctcc 360
ttcaagggaa taaaattttc taagggaaaa tacaaatgtg ttgttgaagc tatttctggg 420
agcccagaag aaatgctctt ttgcttggag tttgtcatcc tacaccaacc taattcaaat 480

<210> 9
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<212> DNA
<213> Homo sapiens

<220>
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<221> mat_peptide
<222> (70)..(501)

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ttt tct tcc ata ttt act gaa gct cag aag cag tat tgg gtc tgc aac 99
Phe Ser Ser Ile Phe Thr Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn
-5 -1 1 5 10

tca tcc gat gca agt att tca tac acc tac tgt gat aaa atg caa tac 147
Ser Ser Asp Ala Ser Ile Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr
15 20 25

cca att tca att aat gtt aac ccc tgt ata gaa ttg aaa gga tcc aaa 195
Pro Ile Ser Ile Asn Val Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys
30 35 40

gga tta ttg cac att ttc tac att cca agg aga gat tta aag caa tta 243
Gly Leu Leu His Ile Phe Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu
45 50 55

tat ttc aat ctc tat ata act gtc aac acc atg aat ctt cca aag cgc 291
Tyr Phe Asn Leu Tyr Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg
60 65 70

aaa gaa gtt att tgc cga gga tct gat gac gat tac tct ttt tgc aga 339
Lys Glu Val Ile Cys Arg Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg
75 80 85 90

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gct ctg aag gga gag act gtg aat aca aca ata tca ttc tcc ttc aag   387
Ala Leu Lys Gly Glu Thr Val Asn Thr Thr Ile Ser Phe Ser Phe Lys
                 95                  100                 105

gga ata aaa ttt tct aag gga aaa tac aaa tgt gtt gtt gaa gct att   435
Gly Ile Lys Phe Ser Lys Gly Lys Tyr Lys Cys Val Val Glu Ala Ile
            110                 115                 120

tct ggg agc cca gaa gaa atg ctc ttt tgc ttg gag ttt gtc atc cta   483
Ser Gly Ser Pro Glu Glu Met Leu Phe Cys Leu Glu Phe Val Ile Leu
        125                 130                 135

cac caa cct aat tca aat tagaataaat tgagtattta aaaaaaaaaa aaaaaaaa 539
His Gln Pro Asn Ser Asn
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<210> 10
<211> 162
<212> PRT
<213> Mus musculus

<400> 10

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Met Asn Gly Val Ala Ala Ala Leu Leu Val Trp Ile Leu Thr Ser Pro
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Ser Ser Ser Asp His Gly Ser Glu Asn Gly Trp Pro Lys His Thr Ala
         -1   1                   5                  10

Cys Asn Ser Gly Gly Leu Glu Val Val Tyr Gln Ser Cys Asp Pro Leu
     15                  20                  25

Gln Asp Phe Gly Leu Ser Ile Asp Gln Cys Ser Lys Gln Ile Gln Ser
 30                  35                  40                  45

Asn Leu Asn Ile Arg Phe Gly Ile Ile Leu Arg Gln Asp Ile Arg Lys
                 50                  55                  60

Leu Phe Leu Asp Ile Thr Leu Met Ala Lys Gly Ser Ser Ile Leu Asn
             65                  70                  75

Tyr Ser Tyr Pro Leu Cys Glu Glu Asp Gln Pro Lys Phe Ser Phe Cys
         80                  85                  90

Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly Pro Val Asn Asn
     95                  100                 105

Pro Gly Leu Asp Val Pro Gln Gly Glu Tyr Gln Leu Leu Leu Glu Leu
110                 115                 120                 125

Tyr Asn Glu Asn Arg Ala Thr Val Ala Cys Ala Asn Ala Thr Val Thr
                130                 135                 140

Ser Ser
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<210> 11
<211> 486

<212> DNA
<213> Mus musculus

<400> 11
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catggcagcg aaaatggttg gcccaagcac acggcctgca acagtggggg cttggaagta 120
gtctaccaga gctgtgatcc cttacaggat tttggccttt ccattgacca gtgttccaag 180
cagatccaat caaatctcaa cattagattt ggcatcattc tgagacagga tatcagaaag 240
ctgtttctgg acataactct gatggcaaaa ggctcttcta ttctgaacta ctcctatccc 300
ctttgtgagg aggaccagcc caagttctca ttctgtggaa gaagaaaagg agaacagata 360
tactatgccg gccctgtcaa taaccctgga cttgatgttc cacagggaga atatcagctc 420
ttgctggaac tgtacaatga aaaccgtgct actgtggctt gtgccaatgc cactgtcacc 480
tcctcc 486

<210> 12
<211> 996
<212> DNA
<213> Mus musculus

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<222> (148)..(576)

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ttaccattgg gcacacacaa ccccctcgcc atg aat ggt gtc gca gct gcc ctc 114
Met Asn Gly Val Ala Ala Ala Leu
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ctt gtg tgg att ctg act tct ccg agc agc agt gac cat ggc agc gaa 162
Leu Val Trp Ile Leu Thr Ser Pro Ser Ser Ser Asp His Gly Ser Glu
-10 -5 -1 1 5

aat ggt tgg ccc aag cac acg gcc tgc aac agt ggg ggc ttg gaa gta 210
Asn Gly Trp Pro Lys His Thr Ala Cys Asn Ser Gly Gly Leu Glu Val
10 15 20

gtc tac cag agc tgt gat ccc tta cag gat ttt ggc ctt tcc att gac 258
Val Tyr Gln Ser Cys Asp Pro Leu Gln Asp Phe Gly Leu Ser Ile Asp
25 30 35

cag tgt tcc aag cag atc caa tca aat ctc aac att aga ttt ggc atc 306
Gln Cys Ser Lys Gln Ile Gln Ser Asn Leu Asn Ile Arg Phe Gly Ile
40 45 50

att ctg aga cag gat atc aga aag ctg ttt ctg gac ata act ctg atg 354
Ile Leu Arg Gln Asp Ile Arg Lys Leu Phe Leu Asp Ile Thr Leu Met
55 60 65

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gca aaa ggc tct tct att ctg aac tac tcc tat ccc ctt tgt gag gag   402
Ala Lys Gly Ser Ser Ile Leu Asn Tyr Ser Tyr Pro Leu Cys Glu Glu
 70                  75                  80                  85

gac cag ccc aag ttc tca ttc tgt gga aga aga aaa gga gaa cag ata   450
Asp Gln Pro Lys Phe Ser Phe Cys Gly Arg Arg Lys Gly Glu Gln Ile
                90                  95                 100

tac tat gcc ggc cct gtc aat aac cct gga ctt gat gtt cca cag gga   498
Tyr Tyr Ala Gly Pro Val Asn Asn Pro Gly Leu Asp Val Pro Gln Gly
            105                 110                 115

gaa tat cag ctc ttg ctg gaa ctg tac aat gaa aac cgt gct act gtg   546
Glu Tyr Gln Leu Leu Leu Glu Leu Tyr Asn Glu Asn Arg Ala Thr Val
        120                 125                 130

gct tgt gcc aat gcc act gtc acc tcc tcc tgagcatggt ctgcaaggaa     596
Ala Cys Ala Asn Ala Thr Val Thr Ser Ser
    135                 140

atgcacagta aactcaatct caggggaccc caaggtccct ggactcacct agctgcaaga 656

accactgata accaagagag gctttacaaa gaaatttctt gtgggtcact cttccgatct 716

tagctccagg gacagatgtt cccagaccca acagatgtaa taaaccctca aaaactatct 776

atttctgagg accctgagta gtcttgaagc cctattgtag tacctctcct tatgtaatta 836

cgtttcatca aagctacttc cttgcctgct ccttagcaac acttccttga agttgcctgg 896

gatgtaaaaa ataaaataaa ataaaataaa ataaaataaa ataaaataaa atgaaatgaa 956

aaataaataa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                      996
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<210> 13
<211> 162
<212> PRT
<213> Homo sapiens

<400> 13

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Met Lys Gly Phe Thr Ala Thr Leu Phe Leu Trp Thr Leu Ile Phe Pro
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Ser Cys Ser Gly Gly Gly Gly Gly Lys Ala Trp Pro Thr His Val Val
            -1   1                  5                  10

Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln Ser Cys Asp Pro Leu
        15                  20                  25

Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser Lys Gln Leu Lys Ser
    30                  35                  40

Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg Glu Asp Ile Lys Glu
45                  50                  55                  60
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Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly Ser Ser Val Leu Asn
                 65                  70                  75

Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro Lys Phe Ser Phe Cys
             80                  85                  90

Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly Pro Val Asn Asn
         95                  100                 105

Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln Val Leu Leu Glu Leu
    110                 115                 120

Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala Asn Ala Thr Ile Met
125                 130                 135                 140

Cys Ser
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<210> 14
<211> 486
<212> DNA
<213> Homo sapiens

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ggcggcggtg ggaaagcctg gcccacacac gtggtctgta gcgacagcgg cttggaagtg 120
ctctaccaga gttgcgatcc attacaagat tttggctttt ctgttgaaaa gtgttccaag 180
caattaaaat caaatatcaa cattagattt ggaattattc tgagagagga catcaaagag 240
ctttttcttg acctagctct catgtctcaa ggctcatctg ttttgaattt ctcctatccc 300
atctgtgagg cggctctgcc caagttttct ttctgtggaa gaaggaaagg agagcagatt 360
tactatgctg ggcctgtcaa taatcctgaa tttactattc ctcagggaga ataccaggtt 420
ttgctggaac tgtacactga aaaacggtcc accgtggcct gtgccaatgc tactatcatg 480
tgctcc 486

<210> 15
<211> 877
<212> DNA
<213> Homo sapiens

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<222> (16)..(75)

<220>
<221> mat_peptide
<222> (76)..(501)

<220>
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<222> (16)..(501)

<400> 15
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                Met Lys Gly Phe Thr Ala Thr Leu Phe Leu Trp Thr
                -20                 -15                 -10
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ctg att ttt ccc agc tgc agt gga ggc ggc ggt ggg aaa gcc tgg ccc   99
Leu Ile Phe Pro Ser Cys Ser Gly Gly Gly Gly Gly Lys Ala Trp Pro
            -5                 -1   1                   5

aca cac gtg gtc tgt agc gac agc ggc ttg gaa gtg ctc tac cag agt  147
Thr His Val Val Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln Ser
     10                  15                  20

tgc gat cca tta caa gat ttt ggc ttt tct gtt gaa aag tgt tcc aag  195
Cys Asp Pro Leu Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser Lys
 25                  30                  35                  40

caa tta aaa tca aat atc aac att aga ttt gga att att ctg aga gag  243
Gln Leu Lys Ser Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg Glu
                45                  50                  55

gac atc aaa gag ctt ttt ctt gac cta gct ctc atg tct caa ggc tca  291
Asp Ile Lys Glu Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly Ser
            60                  65                  70

tct gtt ttg aat ttc tcc tat ccc atc tgt gag gcg gct ctg ccc aag  339
Ser Val Leu Asn Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro Lys
        75                  80                  85

ttt tct ttc tgt gga aga agg aaa gga gag cag att tac tat gct ggg  387
Phe Ser Phe Cys Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly
     90                  95                  100

cct gtc aat aat cct gaa ttt act att cct cag gga gaa tac cag gtt  435
Pro Val Asn Asn Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln Val
105                 110                 115                 120

ttg ctg gaa ctg tac act gaa aaa cgg tcc acc gtg gcc tgt gcc aat  483
Leu Leu Glu Leu Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala Asn
                125                 130                 135

gct act atc atg tgc tcc tgactgtggc ctgtagcaaa aatcacagcc         531
Ala Thr Ile Met Cys Ser
            140

agctgcatct cgtgggacct ccaagctcct ctgactgaac ctactgtggg aggagaagca 591

gctgatgaca gagagaggct ctacaaagaa gcgcccccaa agagtgcagc tgctaatttt 651

agtcccagga ccagacatcc ccagactcca cagatgtaat gaagtccccg aatgtatctg 711

tttctaagga gcctcttggc agtccttaag cagtcttgag ggtccatcct ttttctctaa 771

ttggtcgcct cccaccagac tcacctgctt ttcaactttt taggagtgct tcctcacagt 831

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<210> 16
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SalI-randam
9mer to snythesize a single strand cDNA

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<221> modified_base
<222> (32...40)
<223> "n" represents a, t, c, or g

<400> 16
gagacggtaa tacgatcgac agtaggtcga cnnnnnnnnn 40

<210> 17
<211> 23
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EcoRI adapter

<400> 17
ccgcgaattc tgactaactg att 23

<210> 18
<211> 25
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EcoRI adapter

<400> 18
aatcagttag tcagaattcg cggac 25

<210> 19
<211> 23
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Forward primer

<400> 19
ccgcgaattc tgactaactg att 23

<210> 20
<211> 24
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Reverse primer

<400> 20
gacggtaata cgatcgacag tagg 24

<210> 21
<211> 34
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 3' Race adapter primer

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<210> 22
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<212> DNA
<213> Mus musculus

<220>
<223> OHP106F2 primer

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<210> 23
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<220>
<223> Description of Unknown Organism: Universal Amplification primer

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<223> OHP106F1 primer

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<220>
<223> Description of Unknown Organism: Universal
Amplification primer

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<210> 26
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<220>
<223> XbaI-mouse OHP106F primer

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<212> DNA
<213> Mus musculus

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<223> XbaI-FLAG-mouse OHP106H primer

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<212> DNA
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<220>
<223> XbaI-6His-mouse OHP106H primer

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